2024-01-29 Web Release

Release notes, January 29, 2024

We've made some updates to the ClinVar web site as part of our effort to better support classifications of somatic variants! More information about somatic classifications in ClinVar is available in our blog post and on GitHub.

Changes to the VCV pages

- The summary section at the top of the page is now broken out into three sections for germline classification and two kinds of somatic classifications, clinical impact and oncogenicity.
    - The data that was previously displayed as "Interpretation" is now displayed as "Germline classification".
- The summary section includes a button, or toggle, that lets you view only germline data or only somatic data on the page.
- The tabs for variant details, genes, and conditions were removed. These sections are now directly on the page so that you don't miss any information.
- The table called "Aggregate interpretations per condition" from the Conditions tab is split into two tables called "Conditions - Germline" and "Conditions - Somatic".
- The table called "Submitted interpretations and evidence" has been split into two tables called "Submissions - Germline" and "Submissions - Somatic".
- Functional evidence and citations - also split or not? need a decision.

Changes to ClinVar search results

We've updated the table showing search results in ClinVar to now show more than one type of classification, and to make the other columns more useful.

Several columns may have more than one value, namely Gene, Protein change, Consequence (molecular consequence, e.g. missense or nonsense), Condition. For these, we display one or two values by default; if there are more than that, there is a comment indicating how many more and you can get more information by clicking through to the VCV page.

- The "Variation" column now shows only the title of the ClinVar records; genomic locations are no longer displayed.
- The "Protein change" for the variant is now displayed within the Gene column.
- A column for the "Type" of variant (e.g. SNV or deletion) and the "Consequence" (molecular consequence, e.g. missense or nonsense) was added.
- The column "Clinical significance" was renamed to "Classification".
    - Icons are used to indicate which type of classification is displayed: G for germline, S for somatic clinical impact, and O for oncogenicity.
- "Classification" and "Review status" were combined into a single column. Stars indicate the review status for each aggregate classification.
- The download option for search results now includes more columns of data, including the aggregate classification, aggregate review status, and aggregate date last evaluated for classifications of somatic clinical impact and oncogenicity.
    - The column Clinical significance was renamed Germline classification.
    - The column Review status was renamed Germline review status.
    - Last reviewed was broken out into its own column named Germline date last evaluated.

Changes to E-utilities

The structure of ClinVar's XML file has also been updated to represent classifications of somatic variants. Thus the efetch command within E-utilities for ClinVar has been updated.

Existing efetch queries return XML with the new format.

You can modify your existing queries to return XML with the old format by adding the parameter old_xml=T.

We plan to support both the old and new XML format for a few months, at least through the end of March.

More information about changes to the ClinVar XML and E-utilities is available on GitHub.

Changes to the data

You should not see any changes to data that was on the ClinVar website prior to Jan 29, 2024; you should only see changes to how the data are displayed on the website.

Any data that were previously displayed as "Interpretation" are now displayed as "Germline classification". A small number of those classifications may truly be classifications in the somatic context; our team will contact the appropriate submitters to offer assistance with updating these records.